

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: HANDA, Hiroshi
KAWAGUCHI, Haruma

(ii) TITLE OF THE INVENTION: DRUG-IMMOBILIZED PARTICLES AND A
PROCESS OF PURIFYING PROTEINS

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
- (B) STREET: 130 Water Street
- (C) CITY: Boston
- (D) STATE: MA
- (E) COUNTRY: USA
- (F) ZIP: 02109

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Corless, Peter F
- (B) REGISTRATION NUMBER: 33,860
- (C) REFERENCE/DOCKET NUMBER: 47115

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 617-523-3400
- (B) TELEFAX: 617-523-6440
- (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

10001426-10201

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Gly Leu Asp Trp Val Lys
1 5

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ala Ala Gly Glu Gly Pro Ala Leu Tyr Glu Asp Pro Pro Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:

TOGETHER "1001"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly Ala Val Ala Glu Asp Gly Asp Glu Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Pro Lys Arg Gly Lys Lys Gly Ala Val Ala Glu Asp Gly Asp Glu
1 5 10 15
Leu Arg Thr Glu Pro Glu Ala Lys Lys Ser Lys Thr Ala Ala Lys Lys
20 25 30
Asn Asp Lys Glu Ala Ala Gly Glu Gly Pro Ala Leu Tyr Glu Asp Pro
35 40 45
Pro Asp Gln Lys Thr Ser Pro Ser Gly Lys Pro Ala Thr Leu Lys Ile
50 55 60
Cys Ser Trp Asn Val Asp Gly Leu Arg Ala Trp Ile Lys Lys Lys Gly
65 70 75 80
Leu Asp Trp Val Lys Glu Glu Asp Ala Pro Asp Ile Leu Cys Leu Gln
85 90 95
Glu Thr Lys Lys Cys Ser Glu Asn Lys Leu Pro Ala Glu Leu Gln Glu Leu
100 105 110
Pro Gly Leu Ser His Gln Tyr Trp Ser Ala Pro Ser Asp Lys Glu Gly
115 120 125
Tyr Ser Gly Val Gly Leu Leu Ser Arg Gln Cys Pro Leu Lys Val Ser
130 135 140
Tyr Gly Ile Gly Asp Glu Glu His Asp Gln Glu Gly Arg Val Ile Val
145 150 155 160
Ala Glu Phe Asp Ser Phe Val Leu Val Thr Ala Tyr Val Pro Asn Ala
165 170 175
Gly Arg Gly Leu Val Arg Leu Glu Tyr Arg Gln Arg Trp Asp Glu Ala
180 185 190
Phe Arg Lys Phe Leu Lys Gly Leu Ala Ser Arg Lys Pro Leu Val Leu
195 200 205

10001426-10201

Cys Gly Asp Leu Asn Val Ala His Glu Glu Ile Asp Leu Arg Asn Pro
 210 215 220
 Lys Gly Asn Lys Lys Asn Ala Gly Phe Thr Pro Gln Glu Arg Gln Gly
 225 230 235 240
 Phe Gly Glu Leu Leu Gln Ala Val Pro Leu Ala Asp Ser Phe Arg His
 245 250 255
 Leu Tyr Pro Asn Thr Pro Tyr Ala Tyr Thr Phe Trp Thr Tyr Met Met
 260 265 270
 Asn Ala Arg Ser Lys Asn Val Gly Trp Arg Leu Asp Tyr Phe Leu Leu
 275 280 285
 Ser His Ser Leu Leu Pro Ala Leu Cys Asp Ser Lys Ile Arg Ser Lys
 290 295 300
 Ala Leu Gly Ser Asp His Cys Pro Ile Thr Leu Tyr Leu Ala Leu
 305 310 315

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTCTCTCGAG ATGCCGAAGC GTGGGAAAAA G

31

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

10001426 " 10201

31

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

TAACTAACTA G

11

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

ATTGATTGAT CCTAG

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGCCTCGAG ATGCCAGCCC TGTATGAGGA CC

32

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGCCTCGAG ATGGATTGGG TAAAGGAAGA AGCC

34

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGCCTCGAG ATGCCTTCGG ACAAGGAAGG GT

32

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

10001426110201

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGCCTCGAG ATGTTTGACT CGTTTGTGCT GGTA

34

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Leu Arg Ala Trp Ile Lys Lys Lys Gly Leu Asp Trp Val Lys Glu Glu
1 5 10 15
Ala

1000142610001